

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 9, 2003, 16:24:23 ; Search time 18.4571 Seconds
(without alignments)
98.997 Million cell updates/sec

Title: US-09-905-691-3
Perfect score: 19
Sequence: 1 AEARARRAARARRAARA 19

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size: 0

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database: PIR_76.*

1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	9	47.4	850	2 JC5700	ErbB kinase activa
2	9	47.4	860	2 JC5702	ErbB kinase activa
3	9	47.4	868	2 JC5701	ErbB kinase activa
4	8	42.1	144	2 H72702	hypothetical prote
5	8	42.1	284	2 T34685	ABC-transporter At
6	8	42.1	328	2 H83363	pyoverdine biosynt
7	8	42.1	334	2 E95279	probable [imported
8	8	42.1	395	1 KISMG	galactokinase (EC
9	8	42.1	501	2 T34741	hypothetical prote
10	8	42.1	532	2 E87343	ABC transporter, A
11	8	42.1	2252	2 S06188	genome polyprotein
12	7	36.8	57	2 G84072	hypothetical prote
13	7	36.8	71	2 A13052	hypothetical prote
14	7	36.8	91	2 A87663	hypothetical prote
15	7	36.8	126	2 T52525	tyrosinase co-fact
16	7	36.8	134	2 A26986	hypothetical prote
17	7	36.8	145	2 E75622	hypothetical prote
18	7	36.8	146	2 A23971	hypothetical prote
19	7	36.8	149	2 T39071	60S ribosomal prot
20	7	36.8	149	2 T41324	60S ribosomal prot
21	7	36.8	168	2 T34804	hypothetical prote
22	7	36.8	219	1 XMECAD	deda protein - Esc
23	7	36.8	219	2 A98029	2,2-dialkylglycine
24	7	36.8	229	2 B35173	hypothetical prote
25	7	36.8	231	2 F75459	hypothetical prote
26	7	36.8	248	2 T35233	hypothetical prote
27	7	36.8	255	2 T36243	probable precorrin
28	7	36.8	256	2 T03371	glycine-rich prote
29	7	36.8	276	2 T43203	probable alpha/alp

30 7 36.8 292 2 JE0233 troponin-I - scall
31 7 36.8 307 2 T45274 transcrption fact
32 7 36.8 315 2 G87464 nitrogen regulatio
33 7 36.8 316 2 B70620 hypothetical prote
34 7 36.8 323 2 E86935 conserved hypothet
35 7 36.8 324 2 A87084 conserved hypothet
36 7 36.8 326 2 B87557 hypothetical prote
37 7 36.8 326 2 S27534 hypothetical prote
38 7 36.8 338 2 D85851 probable oxidoredu
39 7 36.8 339 2 F83026 conserved hypothet
40 7 36.8 344 2 H70710 probable hemz prot
41 7 36.8 353 2 T35671 probable transmemb
42 7 36.8 354 2 B57333 G protein-coupled
43 7 36.8 360 2 F70819 probable ionicttran
44 7 36.8 383 2 T35773 succinyl-Coa synth
45 7 36.8 393 2 D70858 probable iron-sulf

RESULT 1

JC5700
ErbB kinase activator alpha, brain and thymus - human
C:Species: Homo sapiens (man)
C:Date: 25-Nov-1997 #sequence_revision 25-Nov-1997 #text_change 08-Sep-2002
C:Accession: JC5700
R:Higashiyama, S.; Horikawa, M.; Yamada, K.; Ichino, N.; Nakano, N.; Nakagawa, T.;
J. Biochem. 122, 675-680, 1997
A:Title: A novel brain-derived member of the epidermal growth factor family that is
A:Reference number: JC5700; MUID:98006324; PMID:9348101
A:Accession: JC5700
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-850 <HIG>
A:Cross-references: DDBJ:AB005060; NID:g2626738; PIDN:BAA23417.1; PID:g2626739
A:Experimental source: SK-NSH cell
C:Comment: This protein is a member of the epidermal growth factor family. It is f
ating the differentiation of MDA-MB-453 cells.
C:Superfamily: human ErbB kinase activator alpha, brain and thymus; EGF homology; f
C:Keywords: glycoprotein
F:258-381/Domain: Ig-like #status predicted <IGL>
F:345-381/Domain: EGF-like #status predicted <EGF>
F:346-381/Domain: EGF-like #status predicted <EGF2>
F:147,278,451/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 47.4% Score 9; DB 2; Length 850;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 EEARARRAA 10

Db 554 EEARARRAA 562

RESULT 2

JC5702
ErbB kinase activator alpha2a, brain and thymus - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 25-Nov-1997 #sequence_revision 25-Nov-1997 #text_change 08-Sep-2002
C:Accession: JC5702; PC4417
R:Higashiyama, S.; Horikawa, M.; Yamada, K.; Ichino, N.; Nakano, N.; Nakagawa, T.;
J. Biochem. 122, 675-680, 1997
A:Title: A novel brain-derived member of the epidermal growth factor family that in
A:Reference number: JC5700; MUID:98006324; PMID:9348101
A:Accession: JC5702
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-860 <HIG>
A:Cross-references: DDBJ:D89996; NID:g2605631; PIDN:BAA23345.1; PID:g2605632
A:Experimental source: PC-12 cell
A:Accession: PC4417
A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA
A:Residues: F, 212-213, 223-860 <H12>
A:Cross-references: DBJ:AB001576; NID:g2605478; PID:BAA23348.1; PID:g2605479
A:Experimental source: PC-12 cell
C:Comment: This protein is a member of the epidermal growth factor family. It is functioning the differentiation of MDA-MB-453 cells.
C:Superfamily: human ErbB kinase activator alpha, brain and thymus; EGF homology; Immunoglobulin-like domain
C:Keywords: glycoprotein
F:274-327/Domain: Ig-like #status predicted <IGL>
F:361-397/Domain: EGF homology <EGF>
F:422-444/Domain: hydrophobic #status predicted <HYD>
F:163,294,467/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 47.4%; Score 9; DB 2; Length 860;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EARRARAA 10
|||||
DB 570 EARRARAA 578

RESULT 3
JC5701
ErbB kinase activator alpha, brain and thymus - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 25-Nov-1997 #sequence_revision 25-Nov-1997 #text_change 08-Sep-2002
C:Accession: JC5701; PC4411
R: Higashiyama, S.; Horikawa, M.; Yamada, K.; Ichino, N.; Nakano, N.; Nakagawa, T.; Miyajima, N.; Bloch, 122, 675-680, 1997
A:Title: A novel brain-derived member of the epidermal growth factor family that interacts with ErbB-2
A:Reference number: JC5700; MUID:98006324; PMID:9348101
A:Accession: JC5701
A:Molecule type: mRNA
A:Residues: 1-868 <H12>
A:Cross-references: DBJ:D89995; NID:g2605629; PID:BAA23344.1; PID:g2605630
A:Accession: PC4411
A:Molecule type: protein
A:Residues: 128-162 <H12>
A:Experimental source: PC-12 cell
C:Comment: This protein is a member of the epidermal growth factor family. It is functioning the differentiation of MDA-MB-453 cells.
C:Superfamily: human ErbB kinase activator alpha, brain and thymus; EGF homology; Immunoglobulin-like domain
F:361-397/Domain: EGF homology <EGF>

Query Match 47.4%; Score 9; DB 2; Length 868;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EARRARAA 10
|||||
DB 578 EARRARAA 586

RESULT 4
H72702
hypothetical protein APE1039 - Aeropyrum pernix (strain K1)
C:Species: Aeropyrum pernix
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C:Accession: H72702
R: Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kikuchi, 6, 83-101, 1999
A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrum pernix
A:Reference number: A72450; MUID:99310339; PMID:10382966
A:Accession: H72702
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-144 <KAW>
A:Cross-references: DBJ:AP000060; NID:g5104188; PID:BAA80024.1; PID:d1043810; PID:g5104188
A:Experimental source: strain K1
C:Genetics:
A:Gene: APE1039

Query Match 42.1%; Score 8; DB 2; Length 144;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 AARRAARA 19
|||||
DB 3 AARRAARA 10

RESULT 5 T34685

ABC-transporter ATP-binding protein - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 17-Mar-2000
C:Accession: T34685
R: Harris, D.; Taylor, K.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, May 1998
A:Reference number: Z21553
A:Accession: T34685
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-284 <HAR>
A:Cross-references: EMBL:AL023517; PIDN:CAA18981.1; GSPDB:GN00070; SCODEB:SC1B5.07
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: SCODEB:SC1B5.07
C:Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology

Query Match 42.1%; Score 8; DB 2; Length 284;
Best Local Similarity 100.0%; Pred. No. 6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 RRAARAA 13
|||||
DB 99 RRAARAA 106

RESULT 6 H83363

providing biosynthesis protein PVCA PA2254 [imported] - Pseudomonas aeruginosa (strain ATCC 27801)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: H83363
R: Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Adam, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: H83363
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-328 <STO>
A:Cross-references: GB:AE004651; GB:AE004091; NID:g9948277; PIDN:AAG05642.1; GSPDB:GN000001
A:Experimental source: strain PA01
C:Genetics:
A:Gene: pvca; PA2254

Query Match 42.1%; Score 8; DB 2; Length 328;
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 ARAARAA 17
|||||
DB 319 ARAARAA 326

RESULT 7 E95279

probable [imported] - Sinorhizobium meliloti (strain 1021) magaplasmid psyna
C:Species: Sinorhizobium meliloti
C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001

C:Accession: E95279
 R:Barrett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows
 : Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.
 Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
 A:Title: Nucleotide sequence and predicted functions of the entire *Sinorhizobium meliloti*
 A:Reference number: A95262; MUID:21396509; PMID:11481432
 A:Accession: E95279
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-334 <KUR>
 A:Cross-references: GB:AE006469; PIDN:AAK64799.1; PID:g14523209; GSPDB:GN00165
 A:Experimental source: strain 1021, megaplasmid pSymA
 R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
 pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
 L.; Hyman, R.W.; Jones, T.
 Science 293, 668-672, 2001
 A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
 hebaull, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
 A:Title: The composite genome of the legume symbiont *Sinorhizobium meliloti*.
 A:Reference number: A96039; MUID:21368234; PMID:11474104
 A:Contents: annotation
 C:Genetics:
 A:Gene: SWA0265
 A:Genome: plasmid
 C:Superfamily: malate dehydrogenase ylbC
 Query Match 42.1%; Score 8; DB 2; Length 334;
 Best Local Similarity 100.0%; Pred. No. 5.8;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 ARARRAAA 10
 DB 306 ARARRAAA 313
 RESULT 8
 KISMG
 galactokinase (EC 2.7.1.6) - Streptomyces sp.
 C:Species: Streptomyces sp.
 C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 28-May-1999
 C:Accession: C28669
 R:Adams, C.W.; Fornwald, J.A.; Schmidt, F.J.; Rosenberg, M.; Brawner, M.E.
 J. Bacteriol. 170, 203-212, 1988
 A:Title: Gene organization and structure of the *Streptomyces lividans* gal operon.
 A:Reference number: A28669; MUID:88086869; PMID:3335481
 A:Accession: C28669
 A:Molecule type: DNA
 A:Residues: 1-395 <ADA>
 A:Cross-references: GB:M18953; NID:g153259; PIDN:AAA26748.1; PID:g153262
 A:Note: the source is designated as *Streptomyces lividans*
 C:Genetics:
 A:Gene: galK
 C:Superfamily: galactokinase
 C:Keywords: ATP; galactose metabolism; phosphotransferase
 Query Match 42.1%; Score 8; DB 1; Length 395;
 Best Local Similarity 100.0%; Pred. No. 7.8;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 9 AARARRA 16
 DB 228 AARARRA 235
 RESULT 9
 T34741
 hypothetical protein SC1E6.20c SC1E6.20c - Streptomyces coelicolor
 C:Species: Streptomyces coelicolor
 C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999
 C:Accession: T34741
 R:Seeger, K.J.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
 submitted to the EMBL Data Library, November 1998
 A:Reference number: Z21555

A:Accession: T34741
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-501 <SEE>
 A:Cross-references: EMBL:AL033505; PIDN:CAA22048.1; GSPDB:GN00070; SCOEDB:SC1E6.20c
 A:Experimental source: strain A3(2)
 C:Genetics:
 A:Gene: SCOEDB:SC1E6.20c
 Query Match 42.1%; Score 8; DB 2; Length 501;
 Best Local Similarity 100.0%; Pred. No. 9.4;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 RARRAAA 11
 DB 71 RARRAAA 78
 RESULT 10
 E87343
 ABC transporter, ATP-binding protein CydC CC0760 [imported] - Caulobacter crescentus
 C:Species: Caulobacter crescentus
 C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
 C:Accession: E87343
 R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg,
 B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Ro
 n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.
 Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
 A:Title: Complete Genome Sequence of *Caulobacter crescentus*.
 A:Reference number: A87249; MUID:21173698; PMID:11259647
 A:Accession: E87343
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-532 <STO>
 A:Cross-references: GB:AE005673; NID:g13421995; PIDN:AAK22745.1; GSPDB:GN00148
 C:Genetics:
 A:Gene: CC0760
 C:Superfamily: Mycobacterium tuberculosis probable ABC transporter cydC; ATP-binding
 Query Match 42.1%; Score 8; DB 2; Length 532;
 Best Local Similarity 100.0%; Pred. No. 9.8;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 ARRAARA 12
 DB 243 ARRAARA 250
 RESULT 11
 S06188
 genome polyprotein 1 - grapevine chrome mosaic virus
 N:Alternate names: RNA1 polyprotein
 N:Contains: cysteine proteinase (EC 3.4.22.-); glycoprotein VPg; nucleotide-binding m
 C:Species: grapevine chrome mosaic virus
 C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 20-Sep-1999
 C:Accession: S06188
 R:Le Gall, O.; Candresse, T.; Brault, V.; Dunez, J.
 Nucleic Acids Res. 17, 7795-7807, 1989
 A:Title: Nucleotide sequence of Hungarian grapevine chrome mosaic nepovirus RNA1.
 A:Reference number: S06188; MUID:90016864; PMID:2798128
 A:Accession: S06188
 A:Molecule type: mRNA
 A:Residues: 1-2252 <LEG>
 A:Cross-references: EMBL:X15346; NID:g59345; PIDN:CAA33405.1; PID:g59346
 A:Note: 1353-Arg and 1870-Arg were also found
 C:Note: the sequence translated from one cDNA differs from that shown in having 1571-
 C:Genetics:
 A:Map position: segment 1
 C:Superfamily: cowpea aphid-borne mosaic virus genome polyprotein B
 C:Keywords: cysteine proteinase; genome-linked protein; hydrolase; membrane protein;
 Query Match 42.1%; Score 8; DB 2; Length 2252;
 Best Local Similarity 100.0%; Pred. No. 31;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 RARRAAAR 11
 Db 249 RARRAAAR 256

RESULT 12

G84072
 hypothetical protein BH3383 [imported] - Bacillus halodurans (strain C-125)
 C:Species: Bacillus halodurans
 C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
 C:Accession: G84072
 R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
 Nucleic Acids Res. 28, 4317-4331, 2000
 A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
 A:Reference number: A83650; MUID:20512582; PMID:11058132
 A:Accession: G84072
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-57 <STO>
 A:Cross-references: GB:AP001518; GB:BA000004; NID:g10175792; PIDN:BA07102.1; GSPDB:GN00
 A:Experimental source: strain C-125
 C:Genetics:
 A:Gene: BH3383

Query Match 36.8%; Score 7; DB 2; Length 57;

Best Local Similarity 100.0%; Pred. No. 11;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 AARRAAR 14
 Db 27 AARRAAR 33

RESULT 13

AI3052
 hypothetical protein Atu4038 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
 C:Species: Agrobacterium tumefaciens
 C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
 C:Accession: AI3052
 R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I
 erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClell
 ; Karp, P.; Romero, P.; Zhang, S.
 Science 294, 2317-2323, 2001
 A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
 ster, E.W.
 A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
 A:Reference number: AB2577; MUID:21608550; PMID:11743193
 A:Accession: AI3052
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-71 <KUR>
 A:Cross-references: GB:AE008689; PIDN:AA144839.1; PID:g17742483; GSPDB:GN00187
 A:Experimental source: strain C58 (Dupont)
 C:Genetics:
 A:Gene: Atu4038
 A:Map position: linear chromosome

Query Match 36.8%; Score 7; DB 2; Length 71;

Best Local Similarity 100.0%; Pred. No. 13;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 RAARRAA 17
 Db 39 RAARRAA 45

RESULT 14

A87663
 hypothetical protein CC3339 [imported] - Caulobacter crescentus
 C:Species: Caulobacter crescentus
 C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001

C:Accession: A87663

R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg,
 B.; Laub, M.T.; Deboy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Ko
 n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C
 Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
 A:Title: Complete Genome Sequence of Caulobacter crescentus.
 A:Reference number: A87249; MUID:21173698; PMID:11259647

A:Accession: A87663

A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-91 <STO>

A:Cross-references: GB:AE005673; NID:g13425039; PIDN:AAK25301.1; GSPDB:GN00148
 C:Genetics:
 A:Gene: CC3339

Query Match 36.8%; Score 7; DB 2; Length 91;

Best Local Similarity 100.0%; Pred. No. 16;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 AARRAR 15
 Db 81 AARRAR 87

RESULT 15

T52525
 tyrosinase co-factor MelC2 [imported] - Streptomyces galbus
 C:Species: Streptomyces galbus
 C:Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 24-Oct-2000
 C:Accession: T52525
 R:Welmeler, U.F.; Brass, N.; Roessler, C.; Piepersberg, W.
 submitted to the EMBL Data Library, February 1996
 A:Description: Cloning and characterization of the mel-operon from Streptomyces galbu
 A:Reference number: Z26098
 A:Accession: T52525
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-126 <WEH>
 A:Cross-references: EMBL:X95705; PIDN:CAA65004.1
 A:Experimental source: DSM40480
 C:Genetics:
 A:Gene: melC1

Query Match 36.8%; Score 7; DB 2; Length 126;

Best Local Similarity 100.0%; Pred. No. 21;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 RAARRAA 13
 Db 105 RAARRAA 111

Search completed: August 9, 2003, 16:34:11
 Job time : 19.4571 secs